

Overview of method for functional site regulatory activity using functional site arrays

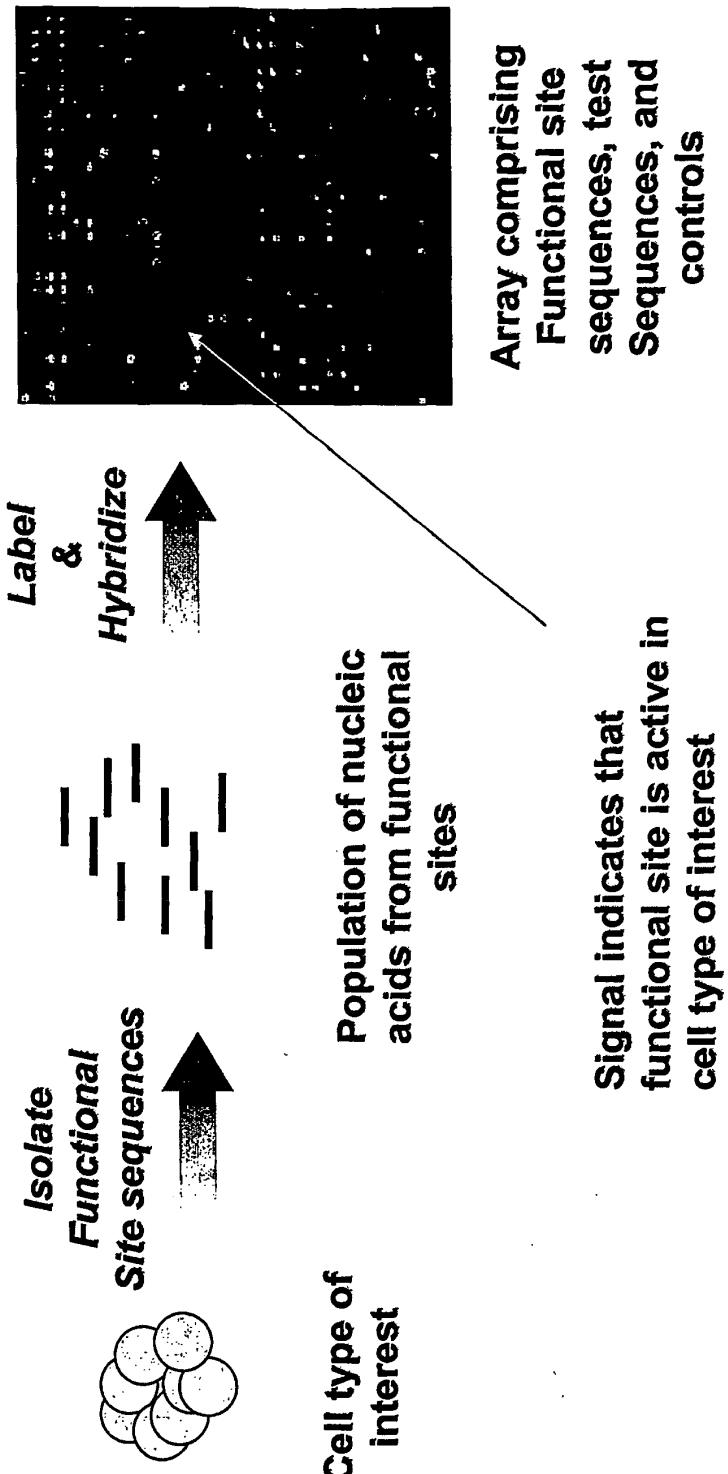
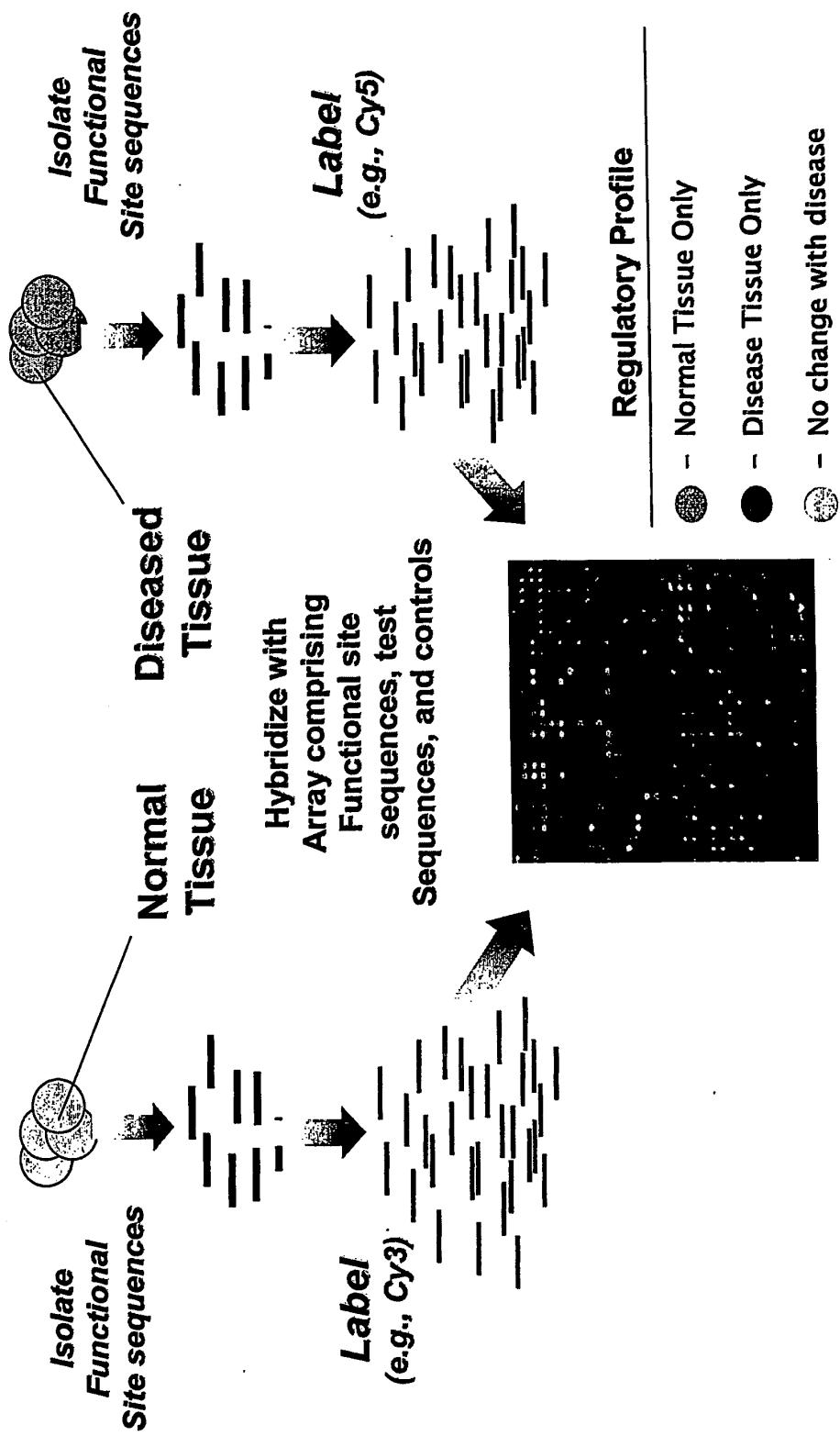


Figure 1

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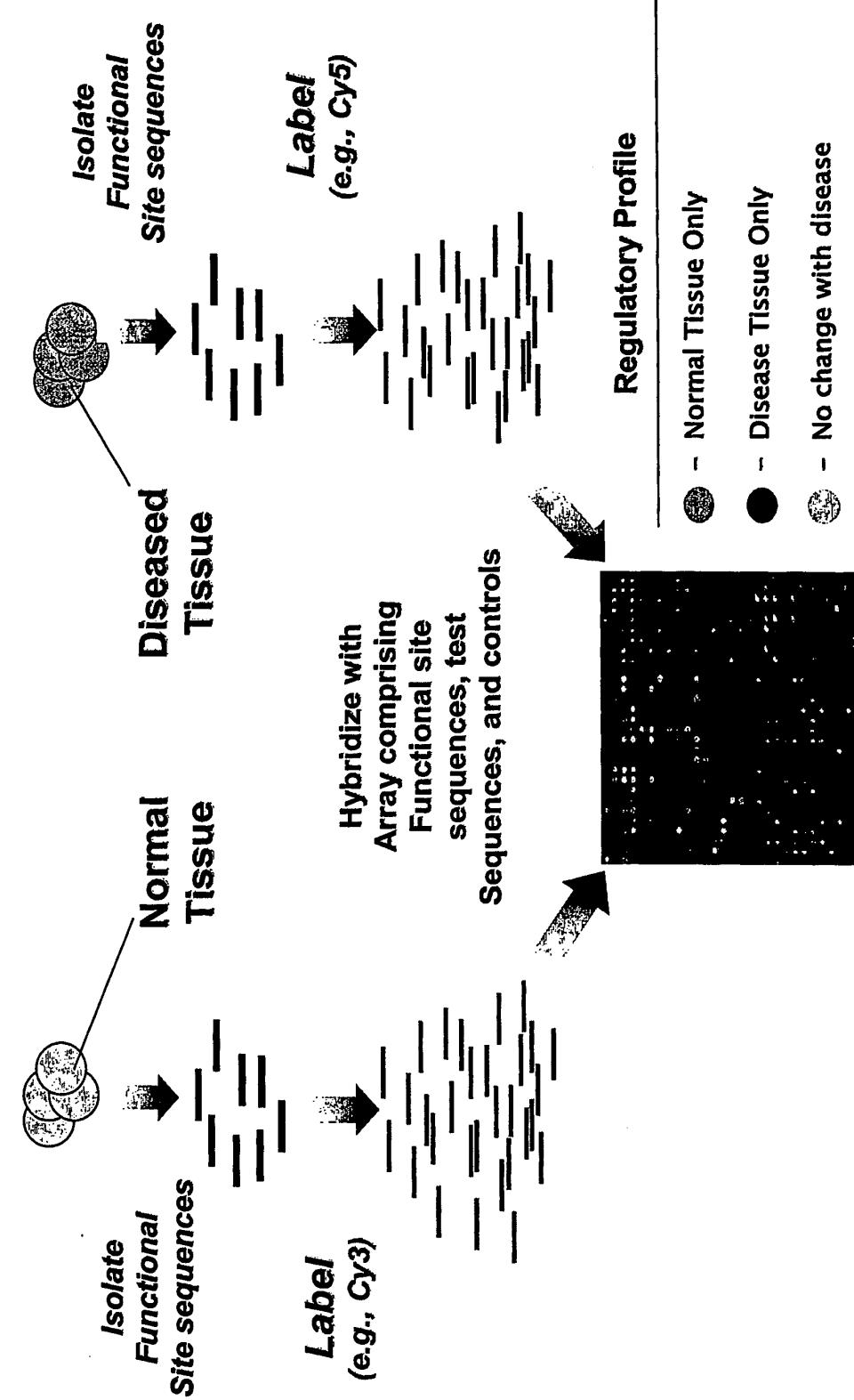
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Figure 2

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Figure 3

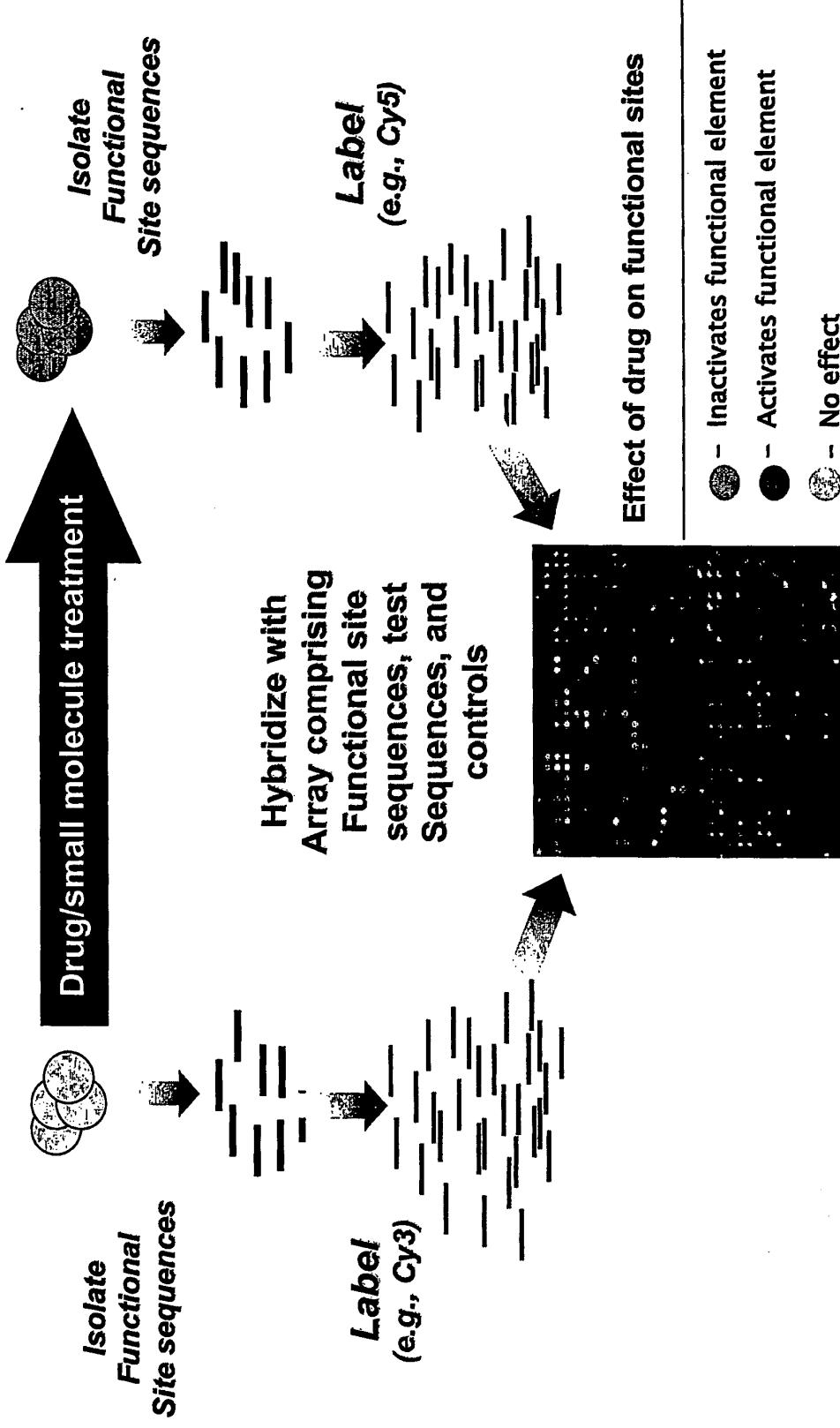


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**Functional Site
Array**

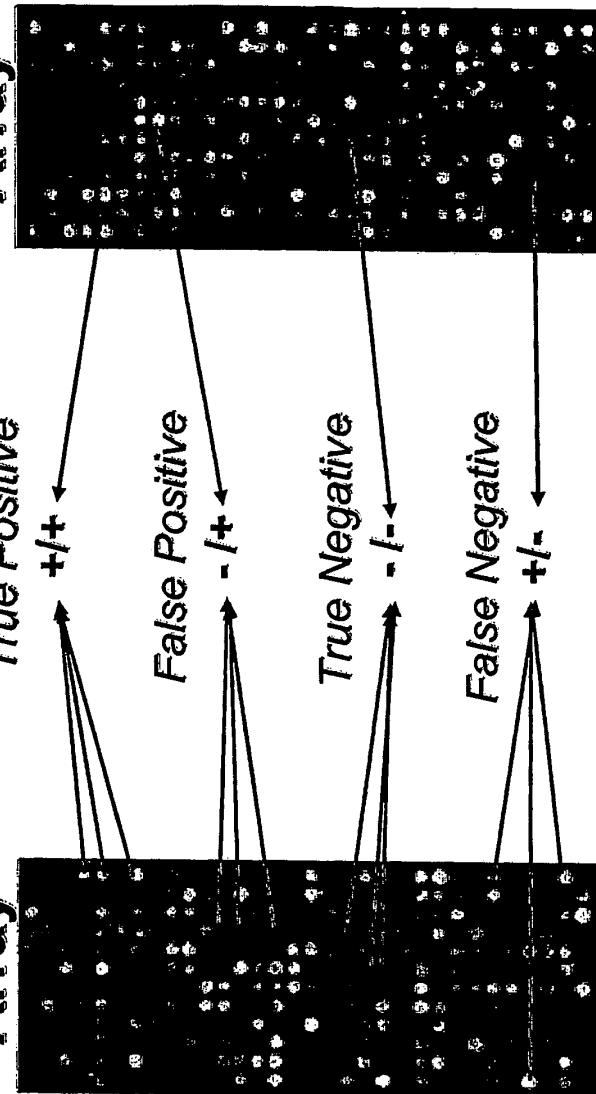


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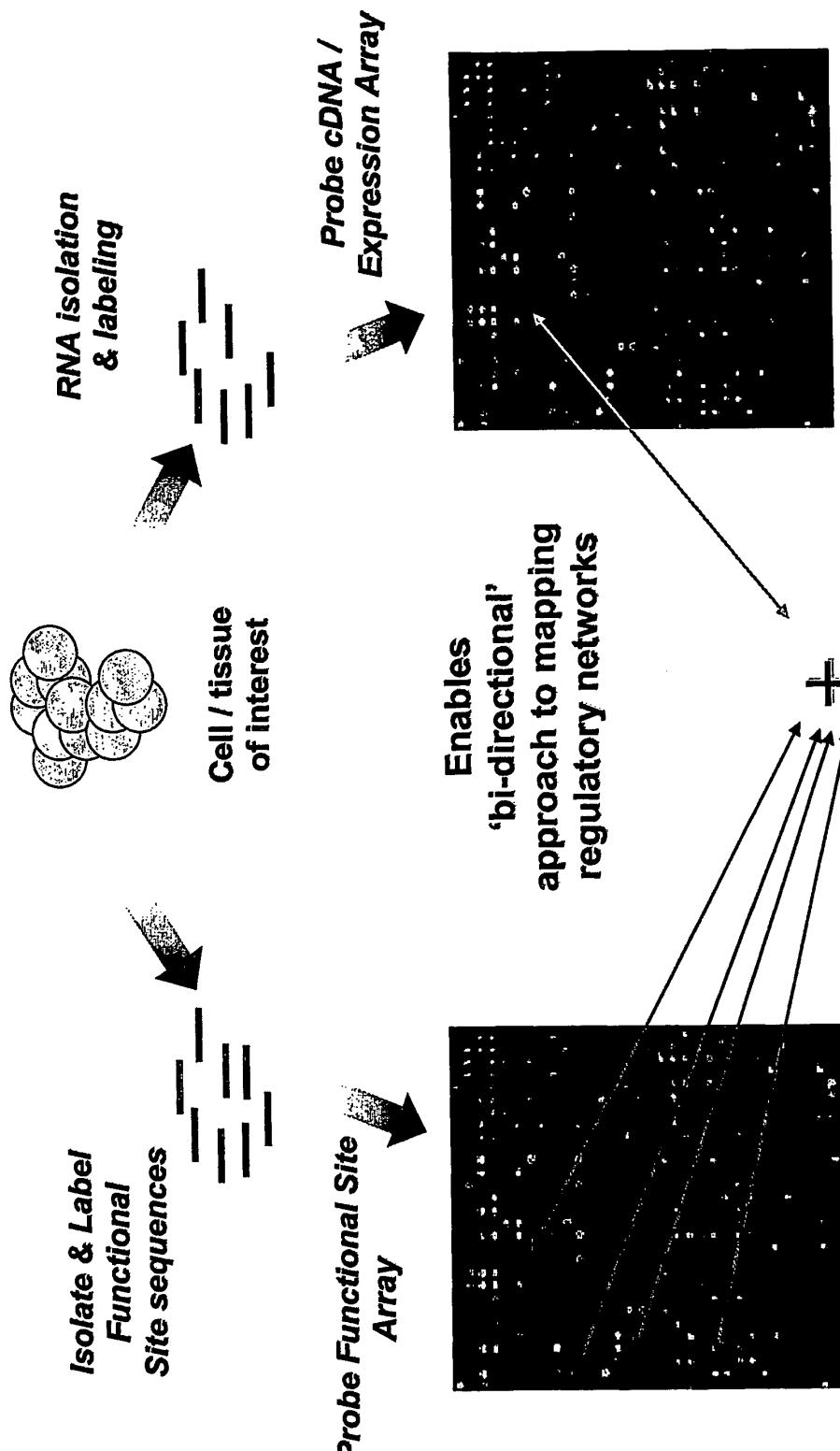


Figure 6

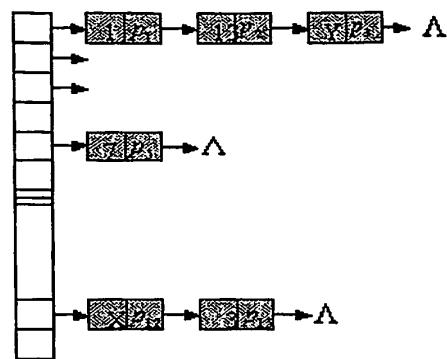


Figure 7

SEQ ID NO:26 GCTGAGAAAACATCAAGGTGTGTTCTCCTCCCCAAAGACACTTCGC

SEQ ID NO:27 AAGCTGTGTTCTCCT 5 50883741 0 Minimum or low frequency 16-mer
SEQ ID NO:27 **AAGCTGTGTTCTCCT X 16 0** Query genome at appropriate
SEQ ID NO:27 AAGCTGTGTTCTCCT Y 19550621 0 positions for *prefix* and *suffix*
SEQ ID NO:28 AGGAGAAAACACAGCTT 4 88449985 1
SEQ ID NO:28 AGGAGAAAACACAGCTT 18 76567666 1
SEQ ID NO:28 AGGAGAAAACACAGCTT 21 33297808 1
SEQ ID NO:28 AGGAGAAAACACAGCTT Y 19088526 1

Figure 8

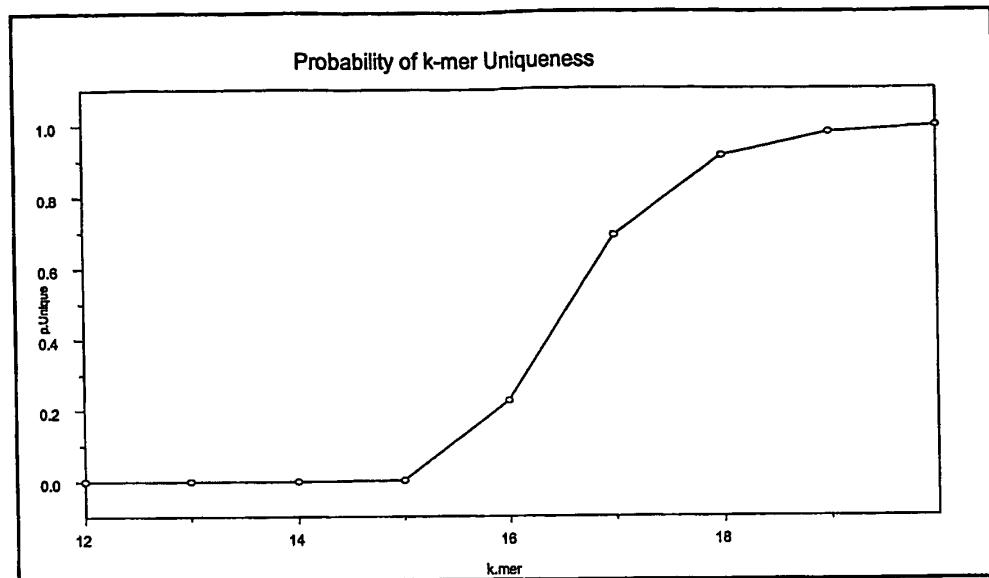


Figure 9

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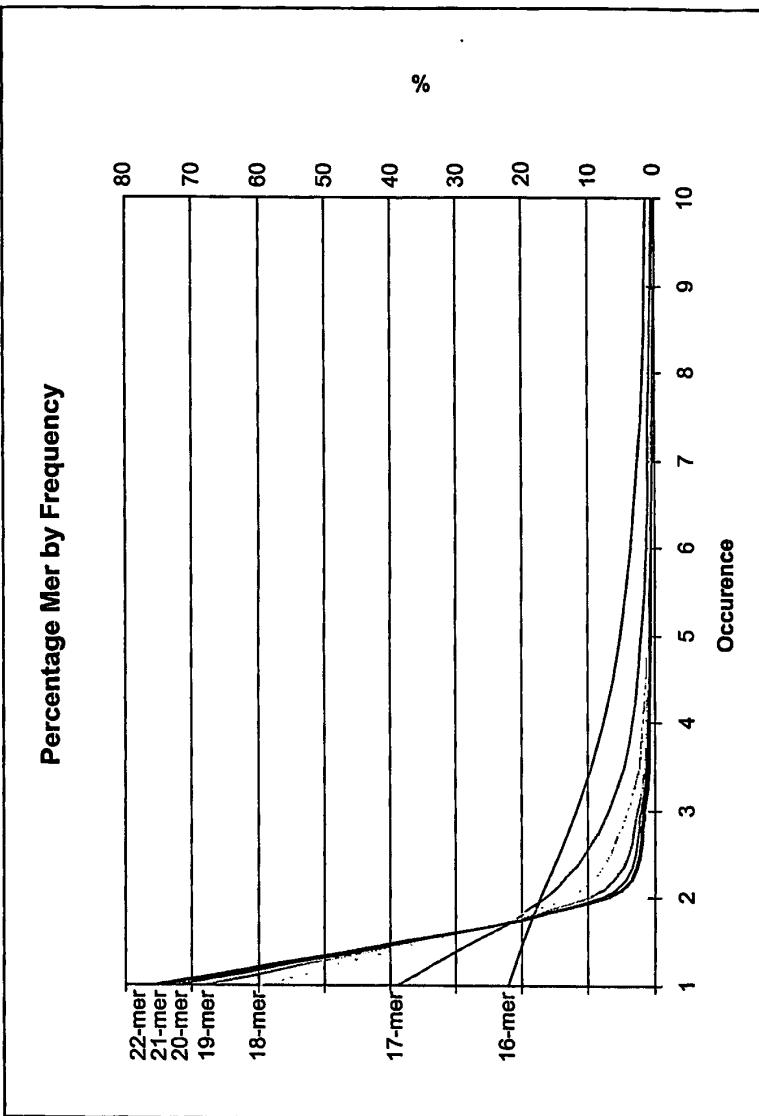
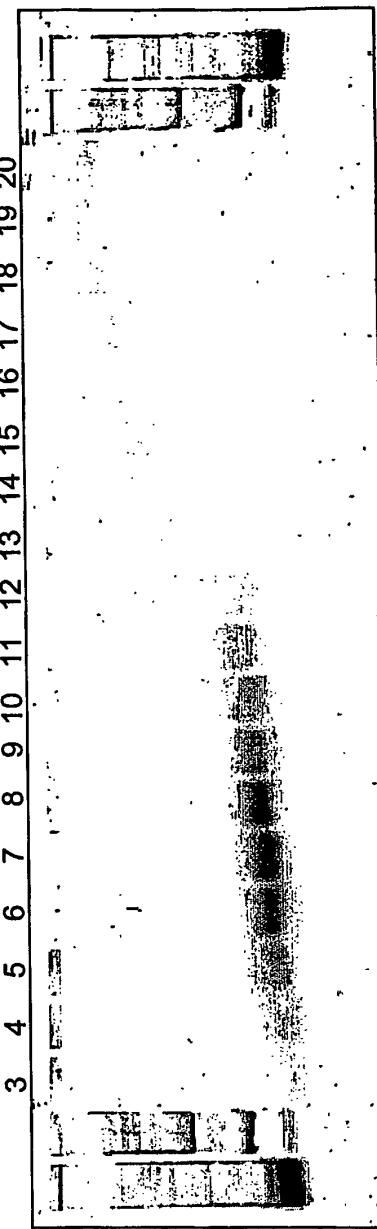


Figure 10

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DNA profile in individual fractions (25 μ l of 6x540 μ l fraction):



Fractions obtained by sucrose-gradient centrifugation 022018 (run #4) of DS-4586 and DS-4587. Run directly from sucrose fractions prior to RNaseA treatment. Total volume of DNA precipitated from fractions and dissolved in LoTE is approx. 80 μ l.

Figure 11

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Correlation between ScanMer(25) scores with Genomic(k562) Hybridization Avg Nsum Intensity

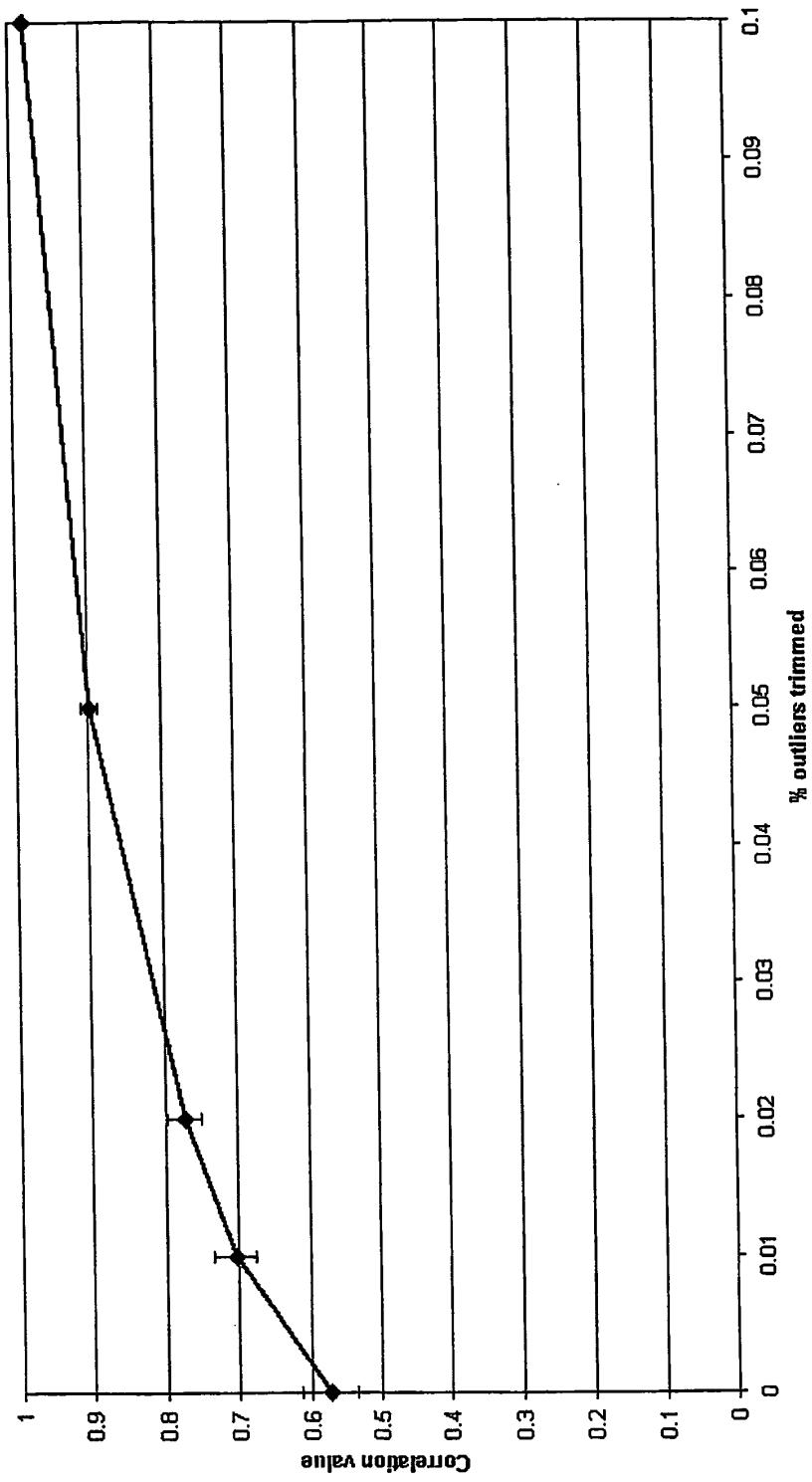


Figure 12

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MYC

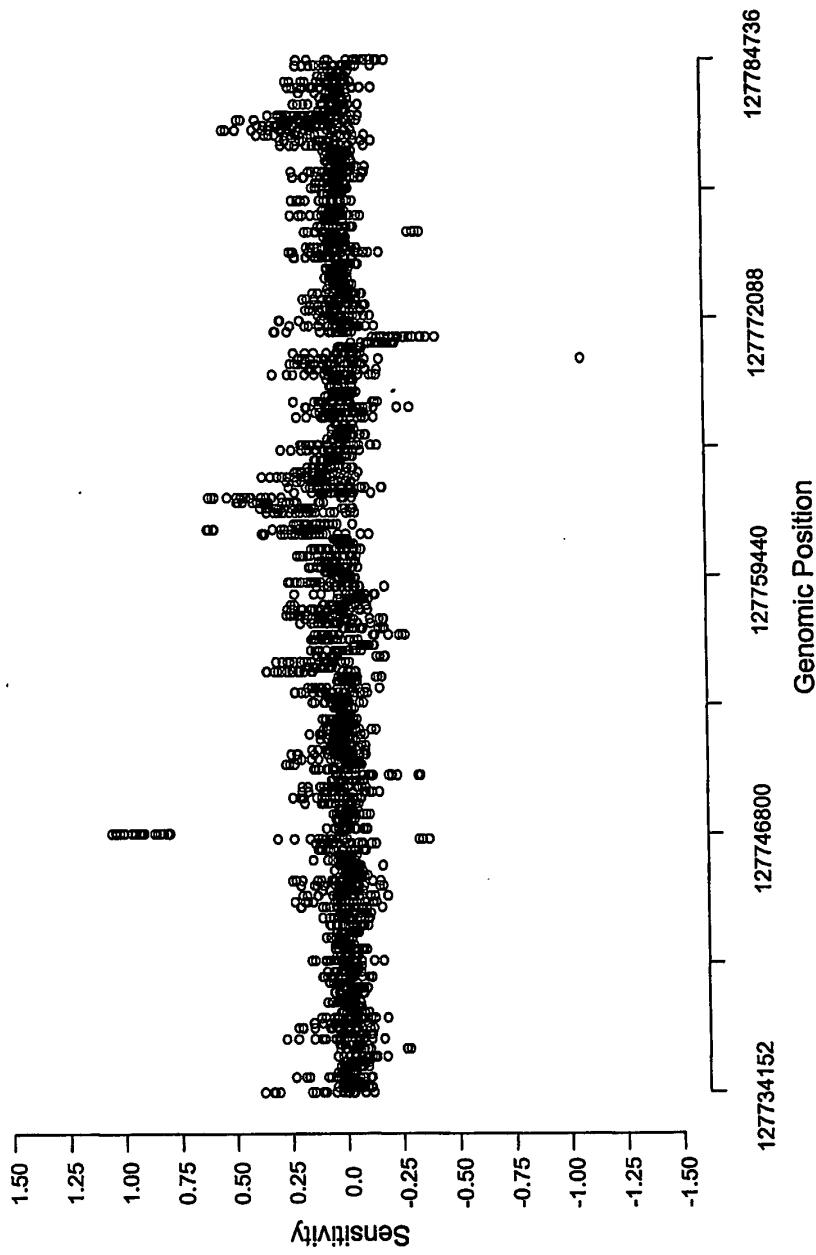


Figure 13.

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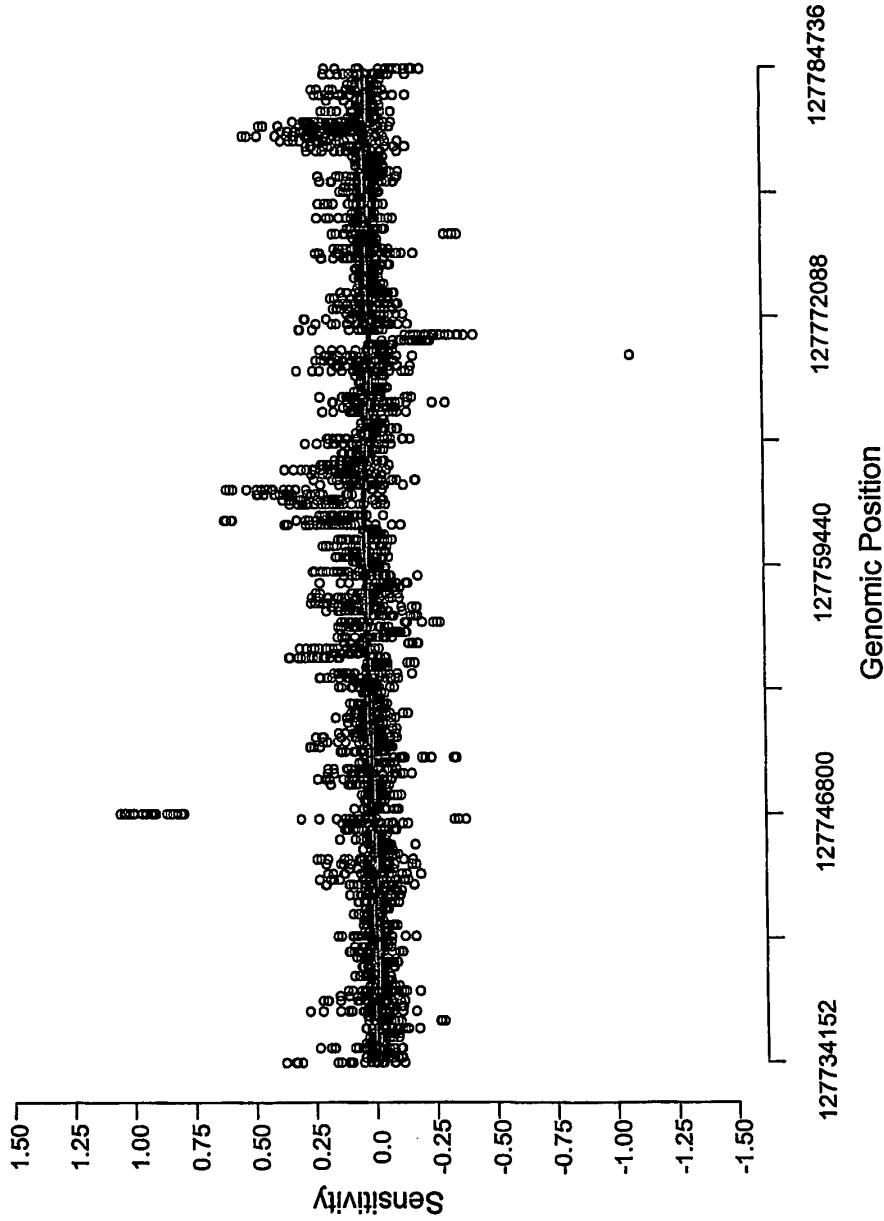


Figure 14.

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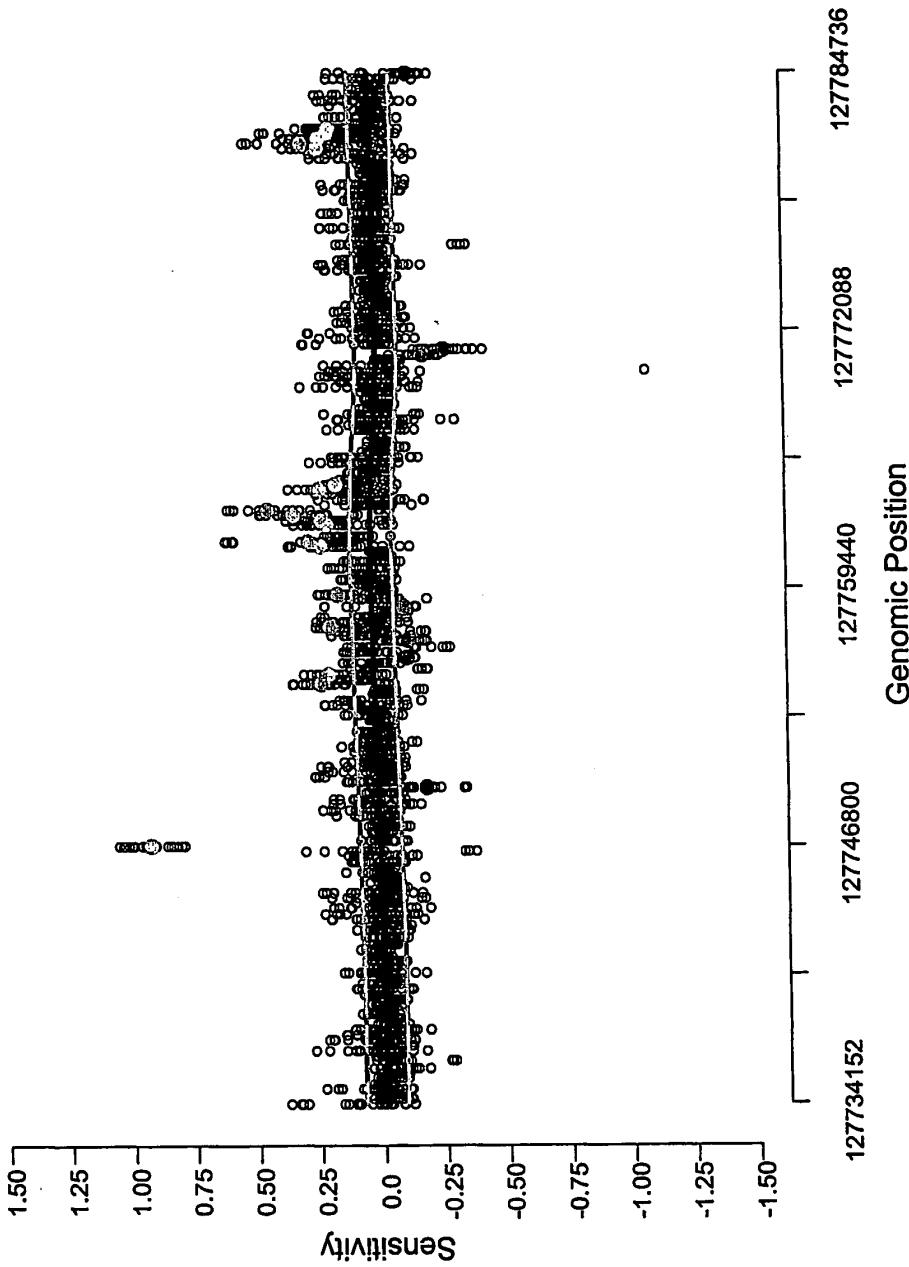


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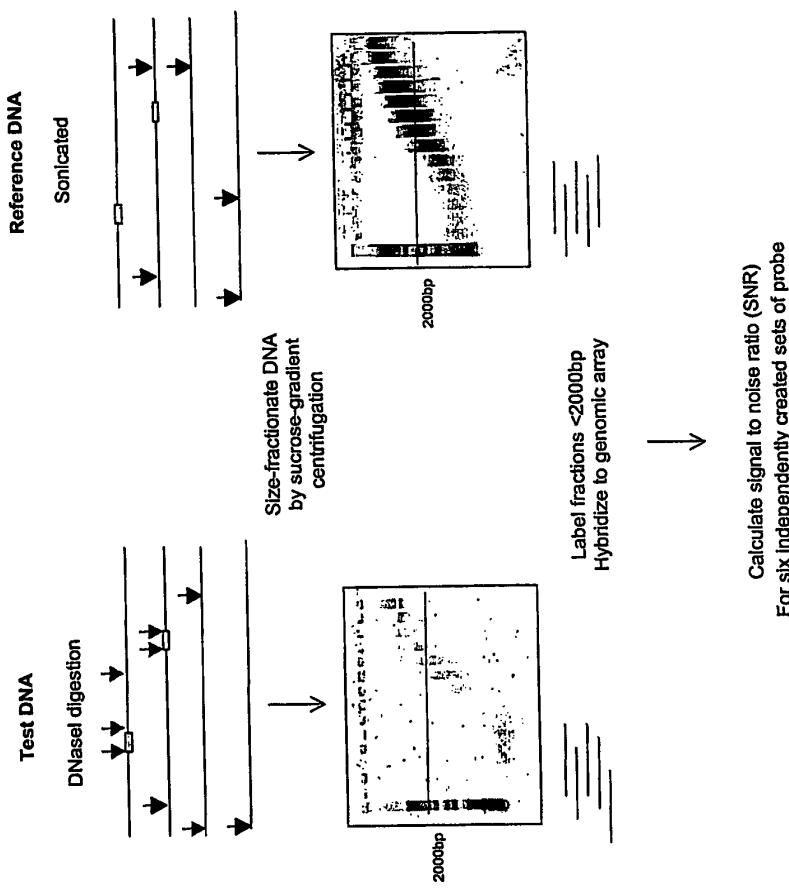


Figure 16.

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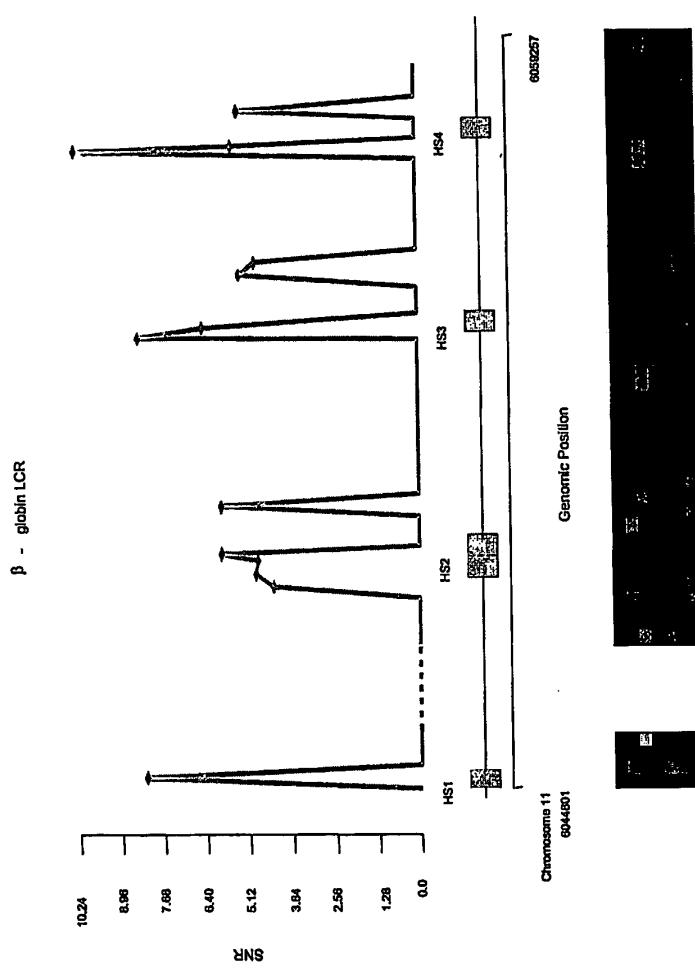


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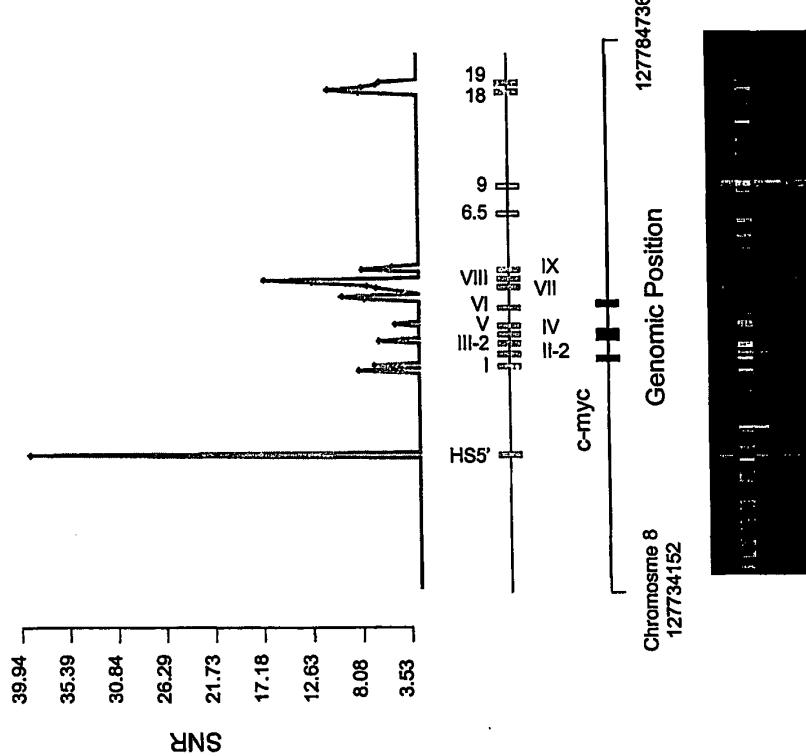


Figure 18.

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